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OM protein - protein search, using sw model

Run on: January 9, 2003, 12:23:23 ; Search time 11 seconds
(without alignments)
49.017 Million cell updates/sec

Title: US-09-632-429-4
Perfect score: 89
Sequence: 1 WEVLCWTWCER 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	48.3	524	1 CP72_CATRO	Q05047 catharanthu
2	43	48.3	536	1 KCN1_RAT	P70606 rattus norv
3	43	48.3	580	1 KCN1_MOUSE	Q9eqr3 mus musculu
4	42	47.2	561	1 KCN1_HUMAN	Q92952 homo sapien
5	42	47.2	569	1 UREL_SYNY3	P73061 synecocyst
6	42	47.2	574	1 KCN2_MOUSE	P58390 mus musculu
7	42	47.2	579	1 KCN2_HUMAN	Q9h2s1 homo sapien
8	42	47.2	580	1 KCN2_RAT	P70604 rattus norv
9	42	47.2	724	1 KCN3_PIG	P58392 sus scrofa
10	42	47.2	731	1 KCN3_MOUSE	P58391 mus musculu
11	42	47.2	732	1 KCN3_RAT	P70605 rattus norv
12	42	47.2	736	1 KCN3_HUMAN	Q9ug16 homo sapien
13	41.5	46.6	359	1 3SHD_NEUCR	P07046 neurospora
14	41	46.1	236	1 SLR1_RALSO	P58590 ralstonia s
15	41	46.1	236	1 SLR2_RALSO	O30919 ralstonia s
16	41	46.1	278	1 RRP1_YEAST	P35178 saccharomyc
17	41	46.1	330	1 QUTG_EMENI	P25416 emericella
18	41	46.1	340	1 QAX_NEUCR	P11634 neurospora
19	41	46.1	416	1 PXN1_XENLA	P49263 xenopus lae
20	41	46.1	809	1 WSKC_DROME	P83097 drosophila
21	40	44.9	295	1 YHK6_YEAST	P38710 saccharomyc
22	40	44.9	741	1 TLE4_RAT	Q07141 rattus norv
23	40	44.9	1080	1 CYA7_HUMAN	P51828 homo sapien
24	39	43.8	471	1 YX11_CAEEL	Q11122 caenorhabdl
25	39	43.8	581	1 YG25_ARCFU	O28648 archaeoglob
26	39	43.8	866	1 I17R_HUMAN	Q96f46 homo sapien
27	39	43.8	1607	1 MIPR_LYMST	Q25410 lymaea sta
28	38.5	43.3	488	1 HDA2_CHICK	P56519 gallus gall
29	38.5	43.3	488	1 HDA2_HUMAN	Q92769 homo sapien
30	38.5	43.3	488	1 HDA2_MOUSE	P70288 mus musculu
31	38	42.7	214	1 VIF_SIVM1	P05903 simian immu
32	38	42.7	214	1 VIF_SIVMK	P05902 simian immu
33	38	42.7	214	1 VIF_SIVS4	P12505 simian immu

34	38	42.7	214	1 VIF_SIVSP	P19506 simian immu
35	38	42.7	215	1 VIF_HV2BE	P18097 human immu
36	38	42.7	215	1 VIF_HV2CA	P24108 human immu
37	38	42.7	215	1 VIF_HV2D1	P17758 human immu
38	38	42.7	215	1 VIF_HV2G1	P16043 human immu
39	38	42.7	215	1 VIF_HV2K1	Q74121 human immu
40	38	42.7	215	1 VIF_HV2N2	P05901 human immu
41	38	42.7	215	1 VIF_HV2RO	P04595 human immu
42	38	42.7	215	1 VIF_HV2SB	P12452 human immu
43	38	42.7	215	1 VIF_HV2ST	P20878 human immu
44	38	42.7	216	1 VIF_HV2D2	P15834 human immu
45	38	42.7	229	1 VIF_CAEVC	P33462 caprine art

ALIGNMENTS

RESULT 1
CP72_CATRO
ID CP72_CATRO STANDARD; PRT; 524 AA.
AC Q05047;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytochrome P450 72A1 (EC 1.14.14.1) (CYPLXXII) (Secologanin synthase)
DE (SLS).
GN CYP72A1 OR CYP72 OR P450CR3
OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
OC Vinceae; Catharanthus.
OX NCBI_TaxID=4058;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. CP3A;
RA Vetter H.-P., Mangold U., Schroeder G., Marner F.-J.,
RA Werck-Reichhart D., Schroeder J.;
RT "Molecular analysis and heterologous expression of an inducible
RT cytochrome P-450 protein from periwinkle (Catharanthus roseus L.).";
RL Plant Physiol. 100:998-1007(1992).
RN [2]
RP SEQUENCE OF 469-524 FROM N.A.
RC STRAIN=cv. G. Don;
RA MEDLINE=93283641; PubMed=8507838;
RA Meijer A.H., Souer E., Verpoorte R., Hoge J.H.C.;
RT "Isolation of cytochrome P-450 cDNA clones from the higher plant
RT Catharanthus roseus by a PCR strategy.";
RL Plant Mol. Biol. 22:379-383(1993).
RN [3]
RP FUNCTION
RC STRAIN=cv. CP3A;
RA MEDLINE=20575722; PubMed=11135113;
RA Irmeler S., Schroeder G., St-Pierre B., Crouch N.P., Hotze M.,
RA Schmidt J., Strack D., Mattern U., Schroeder J.;
RT "Indole alkaloid biosynthesis in Catharanthus roseus: new enzyme
RT activities and identification of cytochrome P450 CYP72A1 as
RT secologanin synthase";
RL Plant J. 24:797-804(2000).
CC -1- FUNCTION: Converts loganin into secologanin.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- PATHWAY: INDOLE ALKALOID SYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Vacuolar membrane (Probable).
CC -1- TISSUE SPECIFICITY: Upper and lower leaf epidermis.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

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CC CONTRIBUTING TO THE SLOW COMPONENT OF SYNAPTIC
CC AFTERHYPERPOLARIZATION. THE CHANNEL IS BLOCKED BY APAMIN (BY
CC SIMILARITY).
CC -!- SUBUNIT: HETERO-OLIGOMER. THE COMPLEX IS COMPOSED OF 4 CHANNEL
CC SUBUNITS EACH OF WHICH BINDS TO A CALMODULIN SUBUNIT WHICH
CC REGULATES THE CHANNEL ACTIVITY THROUGH CALCIUM-BINDING (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: AT LEAST 16 ISOFORMS ARE PRODUCED
CC RESULTING FROM THE DIFFERENTIAL SPLICING OF AT LEAST 12 EXONS.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED INCLUDING BRAIN.
CC -!- POLYMORPHISM: THE POLY-GLU REGION OF KCNN1 IS POLYMORPHIC AND THE
CC NUMBER OF GLN VARIES BETWEEN STRAINS (FROM 10 TO 12). THE REPEAT
CC WITH 10 GLU RESIDUES (SHOWN HERE) IS FOUND IN BALB/C, DBA/2J,
CC 129/SVJ, A/J, C3H/HEJ, BALB/CJ, BXD-31, SM/J, ST/BJ, FVB/NJ,
CC NZB/BNJ, CRA/J AND CAST/EI.
CC -!- SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.
CC
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CC
CC EMBL; AF116525; AAG43216.1; -
CC EMBL; AF297870; AAK30363.1; -
CC EMBL; AF297869; AAK30363.1; JOINED.
CC EMBL; AF303461; AAK29550.1; -
CC EMBL; AF303462; AAK29551.1; -
CC EMBL; AF303463; AAK29552.1; -
CC EMBL; AF357239; AAK48900.1; -
CC HSSP; P70604; IG4Y.
CC MGD; MGI-1933993; Kcnll.
CC InterPro; IPR004178; CamBD.
CC InterPro; IPR001622; K+channel_pore.
CC InterPro; IPR003931; SK_channel.
CC Pfam; PF02888; CamBD; 1.
CC Pfam; PF03530; SK_channel; 1.
CC Ionic channel; Transmembrane; Ion transport; Calmodulin-binding;
KW
KW Alternative splicing; Polymorphism.
FT TRANSMEM 151 171 SEGMENT S1 (POTENTIAL).
FT TRANSMEM 180 200 SEGMENT S2 (POTENTIAL).
FT TRANSMEM 219 239 SEGMENT S3 (POTENTIAL).
FT TRANSMEM 268 288 SEGMENT S4 (POTENTIAL).
FT TRANSMEM 317 337 SEGMENT S5 (POTENTIAL).
FT DOMAIN 357 377 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT DOMAIN 386 406 SEGMENT H6 (POTENTIAL).
FT DOMAIN 107 118 POLY-GLU.
FT DOMAIN 424 503 CALMODULIN-BINDING (BY SIMILARITY).
FT VARSPPLIC 1 43 MISSING (IN EXON A/3.2 OR C/B/3.2).
FT VARSPPLIC 394 430 MISSING (IN EXON 6/8).
FT VARSPPLIC 466 580 KFLQAIHQAKLRSVKIEQGVNDQANTLAELAKAQSIAYE
FT FT VSELAQQOEELAEARLALESRLDVLGSLQALPLGLIAQAI
FT FT CPLPPWPGPHGLATATHSPQSHWLTGMSDCG -> LRSS
FT FT EV (IN EXON 8/10).
FT FT KFLQATHQAKLRSVKIEQGVNDQANTLAELAKAQSIAYE
FT FT VSELAQQOEELAEARLALESRLDVLGSLQALPLGLIAQAI
FT FT CPLPPWPGPHGLATATHSPQSHWLTGMSDCG -> SEV
FT FT (IN EXONS 8/10).
FT FT MISSING (IN EXON 8A/10).
FT FT E -> EE (IN STRAINS C57BL/6J, A/HEJ AND
FT FT SPRET/EI).
FT FT E -> EEE (IN STRAINS SWR/J, AKR/J,
FT FT RBE/DNJ AND P/J).
FT FT H -> Q (IN C57BL/6J).
FT VARIAT 565 580 MW: 7B30C8A28B34C80 CRC64;
FT SEQUENCE 580 AA; 64066 MW; 48.3%; Score 43; DB 1; Length 580;
Best Local Similarity 53.8%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLCTWETCER 13
Db 334 WIVAAMTVRCER 346
RESULT 4
KCNL_HUMAN STANDARD; PRT; 561 AA.
ID KCNN1_HUMAN
AC Q92952;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small conductance calcium-activated potassium channel protein 1 (SK1).
GN KCNN1 OR SK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RX MEDLINE=96376602; PubMed=8781233;
RA Koehler M., Hirschberg B., Bond C.T., Kinzie J.M., Marrion N.V.,
RA Maylie J., Adelman J.P.;
RT "Small-conductance, calcium-activated potassium channels from
mammalian brain".
RL Science 273:1709-1714(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99447612; PubMed=10516439;
RA Litt M., Lamorticella D., Bond C.T., Adelman J.P.;
RT "Gene structure and chromosome mapping of the human small-conductance
calcium-activated potassium channel SK1 gene (KCNN1)".
RL Cytogenet. Cell Genet. 86:70-73(1999).
CC -!- FUNCTION: FORMS A VOLTAGE-INDEPENDENT POTASSIUM CHANNEL ACTIVATED
CC BY INTRACELLULAR CALCIUM. ACTIVATION IS FOLLOWED BY MEMBRANE
CC HYPERPOLARIZATION. THOUGHT TO REGULATE NEURONAL EXCITABILITY BY
CC CONTRIBUTING TO THE SLOW COMPONENT OF SYNAPTIC
CC AFTERHYPERPOLARIZATION. THE CHANNEL IS BLOCKED BY APAMIN.
CC -!- SUBUNIT: HETERO-OLIGOMER. THE COMPLEX IS COMPOSED OF 4 CHANNEL
CC SUBUNITS EACH OF WHICH BINDS TO A CALMODULIN SUBUNIT WHICH
CC REGULATES THE CHANNEL ACTIVITY THROUGH CALCIUM-BINDING (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.
CC
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CC
CC EMBL; U69883; AAB09562.1; -
CC EMBL; AF131948; AAD37507.1; -
CC EMBL; AF131940; AAD37507.1; JOINED.
CC EMBL; AF131942; AAD37507.1; JOINED.
CC EMBL; AF131943; AAD37507.1; JOINED.
CC EMBL; AF131944; AAD37507.1; JOINED.
CC EMBL; AF131945; AAD37507.1; JOINED.
CC EMBL; AF131946; AAD37507.1; JOINED.
CC EMBL; AF131947; AAD37507.1; JOINED.
CC HSSP; P70604; IG4Y.
CC Genew; HGNC:6290; KCNN1.
CC MIM; 602982; -
CC InterPro; IPR004178; CamBD.
CC InterPro; IPR001622; K+channel_pore.
CC InterPro; IPR003931; SK_channel.
CC Pfam; PF02888; CamBD; 1.
CC Pfam; PF03530; SK_channel; 1.
KW Ionic channel; Transmembrane; Ion transport; Calmodulin-binding.

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FT TRANSMEM 129 149 SEGMENT S1 (POTENTIAL).
FT TRANSMEM 158 178 SEGMENT S2 (POTENTIAL).
FT TRANSMEM 197 217 SEGMENT S3 (POTENTIAL).
FT TRANSMEM 246 266 SEGMENT S4 (POTENTIAL).
FT TRANSMEM 295 315 SEGMENT S5 (POTENTIAL).
FT TRANSMEM 335 355 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT DOMAIN 364 384 SEGMENT S6 (POTENTIAL).
FT DOMAIN 402 481 CALMODULIN-BINDING (BY SIMILARITY).
FT DOMAIN 527 536 POLY-PRO.
SQ SEQUENCE 561 AA; 61826 MW; 66CA9A21C5FFDE74 CRC64;

Query Match 47.2%; Score 42; DB 1; Length 561;
Best Local Similarity 46.2%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLCHWTWETCER 13
| : || |||
DB 312 WTIAAWTVRVCER 324

RESULT 5
UREL_SYNY3 STANDARD; PRT; 569 AA.
AC P73061;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Urease alpha subunit (EC 3.5.1.5) (Urease amidohydrolase).
GN UREASE OR SLL1750.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugliura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT 'Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.';
RL DNA Res. 3:109-136(1996).
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -!- COFACTOR: Binds 2 nickel ions per subunit (By similarity).
CC -!- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).
CC -!- PTM: Lys-219 is carbamylated. The carbamoyl group provides the
CC ligands for the two nickel ions (By similarity).
CC -!- SIMILARITY: BELONGS TO THE UREASE FAMILY.
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CC EMBL; D90903; BAAL7083.1; -.
CC HSSP; P18314; LFWE.
CC MEROPS; M38; UNW. -.
CC InterPro; IPR001924; UreaseA.
CC Pfam; PF00449; urease_1.
CC Pfam; PF02802; urease_C; 1.
CC ProDom; PD002467; UreaseA; 1.
CC PROSITE; PS00145; UREASE_2; 1.
CC PROSITE; PS01120; UREASE_1; 1.
CC Hydrolase; Metal-binding; Nickel; Complete proteome.
FT METAL 136 136 NICKEL 2 (BY SIMILARITY).
FT METAL 138 138 NICKEL 2 (BY SIMILARITY).
FT METAL 219 219 NICKEL 1 AND 2 (BY SIMILARITY).
FT METAL 248 248 NICKEL 1 (BY SIMILARITY).
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FT METAL 274 274 NICKEL 1 (BY SIMILARITY).
FT METAL 362 362 NICKEL 2 (BY SIMILARITY).
FT ACT_SITE 322 322 BY SIMILARITY.
SQ SEQUENCE 569 AA; 61037 MW; 1C720A254335D7FD CRC64;

Query Match 47.2%; Score 42; DB 1; Length 569;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVLCWTWETCER 13
||:|||||:
DB 371 EVICRTWQTAHK 382

RESULT 6
KCIN2_MOUSE STANDARD; PRT; 574 AA.
AC P58390;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small conductance calcium-activated potassium channel protein 2 (SK2).
GN KCNN2 OR SK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Colon;
RA MEDLINE=21440983; PubMed=11557517;
RA Ro S., Hatton W.J., Koh S.D., Horowitz B.;
RT "Molecular properties of small-conductance Ca2+-activated K+ channels
RT expressed in murine colonic smooth muscle.";
RL Am. J. Physiol. 281:G964-G973(2001).
CC -!- FUNCTION: FORMS A VOLTAGE-INDEPENDENT POTASSIUM CHANNEL ACTIVATED
CC BY INTRACELLULAR CALCIUM. ACTIVATION IS FOLLOWED BY MEMBRANE
CC HYPERPOLARIZATION. THOUGHT TO REGULATE NEURONAL EXCITABILITY BY
CC CONTRIBUTING TO THE SLOW COMPONENT OF SYNAPTIC
CC AFTERHYPERPOLARIZATION. THE CHANNEL IS BLOCKED BY APAMIN (BY
CC SIMILARITY).
CC -!- SUBUNIT: HETERO-OLIGOMER. THE COMPLEX IS COMPOSED OF 4 CHANNEL
CC SUBUNITS EACH OF WHICH BINDS TO A CALMODULIN SUBUNIT WHICH
CC REGULATES THE CHANNEL ACTIVITY THROUGH CALCIUM-BINDING (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.
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CC EMBL; AF357240; AAK48901.1; -.
CC MGD; MGI:2153182; Kcnn2.
CC InterPro; IPR004178; CamBD.
CC InterPro; IPR001622; K+channel_pore.
CC InterPro; IPR003931; SK_channel.
CC Pfam; PF02888; CamBD; 1.
CC Pfam; PF03530; SK_channel; 1.
CC Ionic channel; Transmembrane; Ion transport; Calmodulin-binding.
FT TRANSMEM 133 153 SEGMENT S1 (POTENTIAL).
FT TRANSMEM 163 183 SEGMENT S2 (POTENTIAL).
FT TRANSMEM 209 229 SEGMENT S3 (POTENTIAL).
FT TRANSMEM 251 271 SEGMENT S4 (POTENTIAL).
FT TRANSMEM 300 320 SEGMENT S5 (POTENTIAL).
FT TRANSMEM 340 360 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT TRANSMEM 369 389 SEGMENT S6 (POTENTIAL).
FT DOMAIN 407 483 CALMODULIN-BINDING (BY SIMILARITY).
FT DOMAIN 42 46 POLY-GLY.
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FT DOMAIN 52 56 POLY-ALA.
 FT DOMAIN 80 85 POLY-GLY.
 FT DOMAIN 88 97 POLY-GLY.
 FT DOMAIN 558 561 POLY-ARG.
 SQ SEQUENCE 574 AA; 63482 MW; 259CB8CDB4D1CDB6 CRC64;
 Query Match 47.2%; Score 42; DB 1; Length 574;
 Best Local Similarity 46.2%; Pred. No. 55;
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 1 WEVLCWTWETCER 13
 | : || |||
 Db 317 WIIAAWTVRACER 329
 | : || |||
 RESULT 7
 KCN2_HUMAN STANDARD; PRT; 579 AA.
 AC Q9H2S1;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Small conductance calcium-activated potassium channel protein 2 (SK2).
 GN KCNN2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20568244; PubMed=10991935;
 RA Desai R., Peretz A., Igelson H., Lazarovici P., Attali B.;
 RT "Ca2+-activated K+ channels in human leukemic Jurkat T cells."
 RT Molecular cloning, biochemical and functional characterization.;
 RL J. Biol. Chem. 275:39954-39963(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Myometrium;
 RA Mazonne J.N., Kaiser R.A., Buxton I.L.O.;
 RT "Characterization of calcium-activated potassium channels in human myometrium."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: FORMS A VOLTAGE-INDEPENDENT POTASSIUM CHANNEL ACTIVATED BY INTRACELLULAR CALCIUM. ACTIVATION IS FOLLOWED BY MEMBRANE HYPERPOLARIZATION. THOUGHT TO REGULATE NEURONAL EXCITABILITY BY CONTRIBUTING TO THE SLOW COMPONENT OF SYNAPTIC AFTERHYPERPOLARIZATION. THE CHANNEL IS BLOCKED BY APAMIN.
 CC -!- SUBUNIT: HETERO-OLIGOMER. THE COMPLEX IS COMPOSED OF 4 CHANNEL SUBUNITS EACH OF WHICH BINDS TO A CALMODULIN SUBUNIT WHICH REGULATES THE CHANNEL ACTIVITY THROUGH CALCIUM-BINDING (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -!- SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.
 CC -----
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 CC -----
 CC EMBL; AF239613; AAG16728.1; -;
 CC DR EMBL; AF397175; AAK84039.1; -;
 CC DR HSP; P70604; 1G4Y.
 CC DR Genew; HGNC:6291; KCNN2.
 CC DR MIM; 605879; -;
 CC DR InterPro; IPR004178; CaMBD.
 CC DR InterPro; IPR001622; K+channel_pore.
 CC DR InterPro; IPR003931; SK_channel.
 CC DR Pfam; PF02888; CaMBD; 1.
 CC DR Pfam; PF03530; SK_channel; 1.

KW Ionic channel; Transmembrane; Ion transport; Calmodulin-binding.
 FT TRANSMEM 138 158 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 168 188 SEGMENT S2 (POTENTIAL).
 FT TRANSMEM 214 234 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 256 276 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 305 325 SEGMENT S5 (POTENTIAL).
 FT TRANSMEM 345 365 SEGMENT S6 (POTENTIAL).
 FT TRANSMEM 374 394 SEGMENT S6 (POTENTIAL).
 FT TRANSMEM 412 488 CALMODULIN-BINDING (BY SIMILARITY).
 FT DOMAIN 41 45 POLY-GLY.
 FT DOMAIN 51 58 POLY-ALA.
 FT DOMAIN 83 88 POLY-GLY.
 FT DOMAIN 91 102 POLY-GLY.
 FT DOMAIN 563 566 POLY-ARG.
 FT CONFLICT 52 52 D -> AA (IN REF. 2).
 FT CONFLICT 323 323 I -> T (IN REF. 2).
 FT CONFLICT 530 530 Q -> R (IN REF. 2).
 SQ SEQUENCE 579 AA; 63803 MW; B1DAE351C106182 CRC64;
 Query Match 47.2%; Score 42; DB 1; Length 579;
 Best Local Similarity 46.2%; Pred. No. 56;
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 1 WEVLCWTWETCER 13
 | : || |||
 Db 322 WIIAAWTVRACER 334
 | : || |||
 RESULT 8
 KCN2_RAT STANDARD; PRT; 580 AA.
 AC P70604;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Small conductance calcium-activated potassium channel protein 2 (SK2).
 GN KCNN2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=56376602; PubMed=8781233;
 RA Koehler M., Hirschberg B., Bond C.T., Kinzie J.M., Marrion N.V., Maylie J., Adelman J.P.;
 RT "Small-conductance, calcium-activated potassium channels from mammalian brain."
 RL Science 273:1709-1714(1996).
 [2]
 RP INTERACTION WITH CALMODULIN.
 RX MEDLINE=98445090; PubMed=9774106;
 RX Xia X.M., Fakler B., Rivard A.F., Wayman G., Johnson-Pals T., Keen J.E., Ishii T., Hirschberg B., Bond C.T., Lutsenko S., Maylie J., Adelman J.P.;
 RA "Mechanism of calcium gating in small-conductance calcium-activated potassium channels."
 RT Nature 395:503-507(1998).
 [3]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 395-490 WITH CALMODULIN.
 RX MEDLINE=21223356; PubMed=1132678;
 RA Schumacher M.A., Rivard A.F., Bachinger H.P., Adelman J.P.;
 RT "Structure of the gating domain of a Ca2+-activated K+ channel complexed with Ca2+/calmodulin."
 RL Nature 410:1120-1124(2001).
 CC -!- FUNCTION: FORMS A VOLTAGE-INDEPENDENT POTASSIUM CHANNEL ACTIVATED BY INTRACELLULAR CALCIUM. ACTIVATION IS FOLLOWED BY MEMBRANE HYPERPOLARIZATION. THOUGHT TO REGULATE NEURONAL EXCITABILITY BY CONTRIBUTING TO THE SLOW COMPONENT OF SYNAPTIC AFTERHYPERPOLARIZATION. THE CHANNEL IS BLOCKED BY APAMIN.
 CC -!- SUBUNIT: HETERO-OLIGOMER. THE COMPLEX IS COMPOSED OF 4 CHANNEL SUBUNITS EACH OF WHICH BINDS TO A CALMODULIN SUBUNIT WHICH

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CC REGULATES THE CHANNEL ACTIVITY THROUGH CALCIUM-BINDING.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U69882; AAB09563.1; -.
DR PDB; 1G4Y; 09-MAY-01.
DR InterPro; IPR004178; CAMBD.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003931; SK_channel.
DR Pfam; PF02888; CAMBD; 1.
DR Pfam; PF03530; SK_channel; 1.
DR Ionic channel; Transmembrane; Ion transport; Calmodulin-binding;
KW 3D-structure.
FT TRANSMEM 140 160 SEGMENT S1 (POTENTIAL).
FT TRANSMEM 169 189 SEGMENT S2 (POTENTIAL).
FT TRANSMEM 215 235 SEGMENT S3 (POTENTIAL).
FT TRANSMEM 257 277 SEGMENT S4 (POTENTIAL).
FT TRANSMEM 306 326 SEGMENT S5 (POTENTIAL).
FT TRANSMEM 346 366 SEGMENT S6 (POTENTIAL).
FT TRANSMEM 375 395 SEGMENT S7 (POTENTIAL).
FT DOMAIN 413 489 CALMODULIN-BINDING.
FT DOMAIN 42 46 POLY-GLY.
FT DOMAIN 52 56 POLY-ALA.
FT DOMAIN 80 85 POLY-GLY.
FT DOMAIN 88 103 POLY-GLY.
FT DOMAIN 564 567 POLY-ARG.
FT SEQUENCE 580 AA; 63847 MW; F71E0DAF7EEFA8D4 CRC64;
SQ SEQUENCE 580 AA; 63847 MW; F71E0DAF7EEFA8D4 CRC64;

Query Match 47.2%; Score 42; DB 1; Length 580;
Best Local Similarity 46.2%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLCTWETCER 13
| : | | |
Db 323 WIIAAWTVRACER 335

RESULT 9
KCNC3_PIG STANDARD; PRT; 724 AA.
AC P58392;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small conductance calcium-activated potassium channel protein 3 (SK3).
GN KCNC3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Coronary artery;
RX MEDLINE=21866175; PubMed=11877319;
RA Burnham M.P., Bychkov R., Feletou M., Richards G.R., Vanhoutte P.M.,
RA Weston A.H., Edwards G.;
RT "Characterization of an apamin-sensitive small-conductance Ca(2+)-
RT activated K(+) channel in porcine coronary artery endothelium:
RT relevance to EDHF.";
RL Br. J. Pharmacol. 135:1133-1143(2002).
CC -1- FUNCTION: FORMS A VOLTAGE-INDEPENDENT POTASSIUM CHANNEL ACTIVATED
CC BY INTRACELLULAR CALCIUM. ACTIVATION IS FOLLOWED BY MEMBRANE
CC HYPERPOLARIZATION. THOUGHT TO REGULATE NEURONAL EXCITABILITY BY
CC CONTRIBUTING TO THE SLOW COMPONENT OF SYNAPTIC

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CC AFTERHYPERPOLARIZATION. THE CHANNEL IS BLOCKED BY APAMIN (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERO-OLIGOMER. THE COMPLEX IS COMPOSED OF 4 CHANNEL
CC SUBUNITS EACH OF WHICH BINDS TO A CALMODULIN SUBUNIT WHICH
CC REGULATES THE CHANNEL ACTIVITY THROUGH CALCIUM-BINDING (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.
CC -----
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CC -----
DR EMBL; AY038049; AAK71498.1; -.
DR InterPro; IPR004178; CAMBD.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003931; SK_channel.
DR Pfam; PF02888; CAMBD; 1.
DR Pfam; PF03530; SK_channel; 1.
DR Ionic channel; Transmembrane; Ion transport; Calmodulin-binding.
KW 3D-structure.
FT TRANSMEM 281 301 SEGMENT S1 (POTENTIAL).
FT TRANSMEM 308 328 SEGMENT S2 (POTENTIAL).
FT TRANSMEM 359 379 SEGMENT S3 (POTENTIAL).
FT TRANSMEM 398 418 SEGMENT S4 (POTENTIAL).
FT TRANSMEM 447 467 SEGMENT S5 (POTENTIAL).
FT TRANSMEM 487 507 SEGMENT S6 (POTENTIAL).
FT TRANSMEM 516 536 SEGMENT S7 (POTENTIAL).
FT DOMAIN 554 630 CALMODULIN-BINDING (BY SIMILARITY).
FT DOMAIN 30 34 POLY-GLN.
FT DOMAIN 35 45 POLY-PRO.
FT DOMAIN 62 73 POLY-GLN.
FT DOMAIN 141 146 POLY-GLY.
FT DOMAIN 676 680 POLY-GLN.
FT DOMAIN 720 723 POLY-SER.
FT SEQUENCE 724 AA; 80372 MW; AFB689A935B4196F CRC64;
SQ SEQUENCE 724 AA; 80372 MW; AFB689A935B4196F CRC64;

Query Match 47.2%; Score 42; DB 1; Length 724;
Best Local Similarity 46.2%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLCTWETCER 13
| : | | |
Db 464 WIIAAWTVRVCER 476

RESULT 10
KCNC3_MOUSE STANDARD; PRT; 731 AA.
AC P58391;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small conductance calcium-activated potassium channel protein 3 (SK3).
GN KCNC3 OR SK3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c; TISSUE=Colon;
RX MEDLINE=21440983; PubMed=11557517;
RA Ro S., Hatton W.J., Koh S.D., Horowitz B.;
RA "Molecular properties of small-conductance Ca2+-activated K+ channels
RA expressed in murine colonic smooth muscle.";
RL Am. J. Physiol. 281:G964-G973(2001).
CC -1- FUNCTION: FORMS A VOLTAGE-INDEPENDENT POTASSIUM CHANNEL ACTIVATED
CC BY INTRACELLULAR CALCIUM. ACTIVATION IS FOLLOWED BY MEMBRANE
CC HYPERPOLARIZATION. THOUGHT TO REGULATE NEURONAL EXCITABILITY BY

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CC CONTRIBUTING TO THE SLOW COMPONENT OF SYNAPTIC
CC AFTERHYPERPOLARIZATION. THE CHANNEL IS BLOCKED BY APAMIN (BY
CC SIMILARITY).
CC -|- SUBUNIT: HETERO-OLIGOMER. THE COMPLEX IS COMPOSED OF 4 CHANNEL
CC SUBUNITS EACH OF WHICH BINDS TO A CALMODULIN SUBUNIT WHICH
CC REGULATES THE CHANNEL ACTIVITY THROUGH CALCIUM-BINDING (BY
CC SIMILARITY).
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -|- SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.
CC -----
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CC -----
DR EMBL; AF357241; AAK48902.1; -.
DR MGD; MGI-2153183; Kcnn3.
DR InterPro; IPR004178; CaMBD.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003931; SK_channel.
DR Pfam; PF02888; CaMBD; 1.
DR Pfam; PF03530; SK_channel; 1.
KW Ionic channel; Transmembrane; Ion transport; Calmodulin-binding.
FT TRANSMEM 288 308 SEGMENT S1 (POTENTIAL).
FT TRANSMEM 315 335 SEGMENT S2 (POTENTIAL).
FT TRANSMEM 366 386 SEGMENT S3 (POTENTIAL).
FT TRANSMEM 405 425 SEGMENT S4 (POTENTIAL).
FT TRANSMEM 454 474 SEGMENT S5 (POTENTIAL).
FT TRANSMEM 494 514 SEGMENT S6 (POTENTIAL).
FT TRANSMEM 523 543 SEGMENT S6 (POTENTIAL).
FT DOMAIN 561 637 CALMODULIN-BINDING (BY SIMILARITY).
FT DOMAIN 30 35 POLY-GLN.
FT DOMAIN 36 43 POLY-PRO.
FT DOMAIN 60 79 POLY-GLN.
FT DOMAIN 683 687 POLY-GLN.
FT DOMAIN 727 730 POLY-SER.
SQ SEQUENCE 731 AA; 81255 MW; E509C97E975C1A42 CRC64;

Query Match 47.2%; Score 42; DB 1; Length 731;
Best Local Similarity 46.2%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLQWTWETCER 13
DB 471 WIIAATVRCER 63

RESULT 11
KCN3_RAT STANDARD; PRT; 732 AA.
AC P70605; Q9EQ81; Q9EQ84;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small conductance calcium-activated potassium channel protein 3 (SK3).
GN KCNN3 OR SK3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=96376602; PubMed=8781233;
RA Koehler M., Hirschberg B., Bond C.T., Kinzie J.M., Marrión N.V.,
RA Maylie J., Adelman J.P.;
RT "Small-conductance, calcium-activated potassium channels from
RL mammalian brain.";
RL Science 273:1709-1714(1996).
RN [2]
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RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21424375; PubMed=11533126;
RA Hosseini R., Benton D.C., Dunn P.M., Jenkinson D.H., Moss G.W.;
RT "SK3 is an important component of K(+) channels mediating the
RT afterhyperpolarization in cultured rat SCG neurons.";
RL J. Physiol. (Lond) 535:323-334(2001).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT 78-GLN-GLN-79 DEL.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=21143871; PubMed=11245600;
RA Barford E.T., Moore A.L., Lidofsky S.D.;
RT "Cloning and functional expression of a liver isoform of the small
RT conductance Ca2+-activated K+ channel SK3.";
RL Am. J. Physiol. 280:C836-C842(2001).
CC -|- FUNCTION: FORMS A VOLTAGE-INDEPENDENT POTASSIUM CHANNEL ACTIVATED
CC BY INTRACELLULAR CALCIUM. ACTIVATION IS FOLLOWED BY MEMBRANE
CC HYPERPOLARIZATION. THOUGHT TO REGULATE NEURONAL EXCITABILITY BY
CC CONTRIBUTING TO THE SLOW COMPONENT OF SYNAPTIC
CC AFTERHYPERPOLARIZATION. THE CHANNEL IS BLOCKED BY APAMIN.
CC -|- SUBUNIT: HETERO-OLIGOMER. THE COMPLEX IS COMPOSED OF 4 CHANNEL
CC SUBUNITS EACH OF WHICH BINDS TO A CALMODULIN SUBUNIT WHICH
CC REGULATES THE CHANNEL ACTIVITY THROUGH CALCIUM-BINDING (BY
CC SIMILARITY).
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -|- SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.
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CC -----
DR EMBL; U69884; AAB81653.1; -.
DR EMBL; AF292389; AAG13967.1; -.
DR EMBL; AF284345; AAG38878.1; -.
DR HSP; P70604; IG4Y.
DR InterPro; IPR004178; CaMBD.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003931; SK_channel.
DR Pfam; PF02888; CaMBD; 2.
DR Pfam; PF03530; SK_channel; 1.
KW Ionic channel; Transmembrane; Ion transport; Calmodulin-binding;
KW Polymorphism.
FT TRANSMEM 289 309 SEGMENT S1 (POTENTIAL).
FT TRANSMEM 316 336 SEGMENT S2 (POTENTIAL).
FT TRANSMEM 367 387 SEGMENT S3 (POTENTIAL).
FT TRANSMEM 406 426 SEGMENT S4 (POTENTIAL).
FT TRANSMEM 455 475 SEGMENT S5 (POTENTIAL).
FT TRANSMEM 495 515 SEGMENT S6 (POTENTIAL).
FT TRANSMEM 524 544 SEGMENT S6 (POTENTIAL).
FT TRANSMEM 562 638 CALMODULIN-BINDING (BY SIMILARITY).
FT DOMAIN 30 35 POLY-GLN.
FT DOMAIN 36 39 POLY-PRO.
FT DOMAIN 60 80 POLY-GLN.
FT DOMAIN 684 688 POLY-GLN.
FT DOMAIN 728 731 POLY-SER.
FT VARIANT 78 79 MISSING.
FT CONFLICT 9 9 D -> E (IN REF. 1).
FT CONFLICT 96 96 L -> V (IN REF. 1).
FT CONFLICT 138 138 L -> V (IN REF. 1).
FT CONFLICT 162 162 L -> V (IN REF. 1).
FT CONFLICT 190 190 S -> N (IN REF. 1).
SQ SEQUENCE 732 AA; 81448 MW; C44579B78EFB6ADA CRC64;

Query Match 47.2%; Score 42; DB 1; Length 732;
Best Local Similarity 46.2%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLQWTWETCER 13
| : || |||
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Db 472 WIIAAWTVRCER 484
RESULT 12
KC3_HUMAN
ID KC3_HUMAN STANDARD; PRT; 736 AA.
AC Q9UGI6; O43517;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small conductance calcium-activated potassium channel protein 3 (SK3)
DE (SKCa3).
DE KCNN3 OR K3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND POLYMORPHISM OF POLY-GLN REGION.
RX MEDLINE=98150774; PubMed=9491810;
RA Chandy K.G., Fantino E., Wittekindt O., Kalman K., Tong L.-L.,
RA Ho T.-H., Gutman G.A., Crocq M.-A., Ganguli R., Ningaonkar V.,
RA Morris-Rosendahl D.J., Gargus J.J.;
RT "Isolation of a novel potassium channel gene hSKCa3 containing a
RT polymorphic CAG repeat: a candidate for schizophrenia and bipolar
RT disorder?";
RL Mol. Psych. 3:32-37(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Terstappen G.C., Pula G., Chen M.X., Roncarati R.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21392854; PubMed=11501944;
RA Sun G., Tomita H., Shakkottai V.G., Gargus J.J.;
RT "Genomic organization and promoter analysis of human KCNN3 gene.";
RL J. Hum. Genet. 46:463-470(2001).
CC -1- FUNCTION: FORMS A VOLTAGE-INDEPENDENT POTASSIUM CHANNEL ACTIVATED
CC BY INTRACELLULAR CALCIUM. ACTIVATION IS FOLLOWED BY MEMBRANE
CC HYPERPOLARIZATION. THOUGHT TO REGULATE NEURONAL EXCITABILITY BY
CC CONTRIBUTING TO THE SLOW COMPONENT OF SYNAPTIC
CC AFTERHYPERPOLARIZATION. THE CHANNEL IS BLOCKED BY APAMIN.
CC -1- SUBUNIT: HETERO-OLIGOMER. THE COMPLEX IS COMPOSED OF 4 CHANNEL
CC SUBUNITS EACH OF WHICH BINDS TO A CALMODULIN SUBUNIT WHICH
CC REGULATES THE CHANNEL ACTIVITY THROUGH CALCIUM-BINDING (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- POLYMORPHISM: THE SECOND POLY-GLN REGION OF KCNN3 IS HIGHLY
CC POLYMORPHIC AND THE NUMBER OF GLN VARIES IN THE POPULATION (FROM
CC 12 TO 28).
CC -1- SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.
CC
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CC
CC EMBL; AF031815; AAC26099.1; -
CC EMBL; AJ251016; CAB61331.1; -
CC EMBL; AF336797; AAK15345.1; -
CC HSSP; P70604; 1G4Y.
CC Genew; HGNC:6292; KCNN3.
CC MIM; 602983; -
CC InterPro; IPR004178; CaMBD.
CC InterPro; IPR001622; K+channel_pore.
CC InterPro; IPR003931; SK_channel.
CC Pfam; PF02888; CaMBD; 2.
CC Pfam; PF03530; SK_channel; 1.
CC Ionic channel; Transmembrane; Ion transport; Calmodulin-binding;
CC Polymorphism.

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FT TRANSMEM 293 313 SEGMENT S1 (POTENTIAL).
FT TRANSMEM 320 340 SEGMENT S2 (POTENTIAL).
FT TRANSMEM 371 391 SEGMENT S3 (POTENTIAL).
FT TRANSMEM 410 430 SEGMENT S4 (POTENTIAL).
FT TRANSMEM 459 479 SEGMENT S5 (POTENTIAL).
FT TRANSMEM 499 519 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT TRANSMEM 528 548 SEGMENT S6 (POTENTIAL).
FT DOMAIN 566 642 CALMODULIN-BINDING (BY SIMILARITY).
FT DOMAIN 30 41 POLY-GLN.
FT DOMAIN 42 48 POLY-PRO.
FT DOMAIN 65 85 POLY-GLN.
FT DOMAIN 688 692 POLY-GLN.
FT DOMAIN 732 735 POLY-SER.
FT VARIANT 81 MISSING.
FT CONFLICT 254 254 /FTID=VAR_012204.
FT CONFLICT 281 281 T -> A (IN REF. 1).
FT CONFLICT 347 347 L -> P (IN REF. 1).
FT CONFLICT 347 347 V -> A (IN REF. 1).
FT CONFLICT 485 485 V -> A (IN REF. 1).
SQ SEQUENCE 736 AA; 82025 MW; CCD0CC1621FFAE9C CRC64;

Query Match 47.28; Score 42; DB 1; Length 736;
Best Local Similarity 46.28; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 13
I : || |||
Db 476 WIIAAWTVRCER 488

RESULT 13
3SHD_NEUCR
ID 3SHD_NEUCR STANDARD; PRT; 359 AA.
AC P07046;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-dehydroshikimate dehydratase (EC 4.2.1.-) (DHS dehydratase)
DE (DHSase).
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A;
RX MEDLINE=89293848; PubMed=2525625;
RA Geever R.F., Huett L., Baum J.A., Tyler B.M., Patel V.B.,
RA Rutledge B.J., Case M.E., Giles N.H.;
RT "DNA sequence, organization and regulation of the qa gene cluster of
RT Neurospora crassa.";
RL J. Mol. Biol. 207:15-34(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85155494; PubMed=6241580;
RA Rutledge B.J.;
RT "Molecular characterization of the qa-4 gene of Neurospora crassa.";
RL Gene 32:275-287(1984).
CC -1- FUNCTION: CONVERTS DEHYDROSHIKIMATE TO PROTOCATECHUATE.
CC -1- PATHWAY: QUINIC ACID CATABOLIC PATHWAY; THIRD STEP. THIS PATHWAY
CC ALLOWS GROWTH OF BACTERIA WITH QUINATE BY ITS CONVERSION TO
CC PROTOCATECHUATE AND SUBSEQUENT METABOLISM BY THE BETA-KETOADIPATE
CC PATHWAY.
CC
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CC

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DR EMBL; X14603; CAA32750.1; -.
DR EMBL; M10139; AAA33613.1; -.
DR PIR; A22421; A22421.
DR PIR; S04252; S04252.
DR PIR; D31277; D31277.
KW Quinate metabolism; Lyase.
SQ SEQUENCE 359 AA; 40493 MW; AF3111E617320F12 CRC64;

Query Match 46.6%; Score 41.5; DB 1; Length 359;
Best Local Similarity 43.8%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

Qy 1 WEVLCWT-----WETC 11
:| |||: |||
Db 164 YESLCWSTRVDLWERC 179

RESULT 14
SLR2_RALSO
ID SLR2_RALSO STANDARD; PRT; 236 AA.
AC P58590;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transcriptional activator protein solR.
GN SOLR OR RSC3287 OR RS02516.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billaut A., Brottier P., Camus J.C., Catolico L.,
Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002)
CC -!- SIMILARITY: BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL
REGULATORS. AUTOINDUCER REGULATED SUBFAMILY.

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CC EMBL; AL646074; CAD17075.1; -.
DR InterPro; IPR005143; Autoind_bind.
DR InterPro; IPR000792; HTH_LuxR.
DR Pfam; PF03472; Autoind_bind; 1.
DR ProDom; PD000307; HTH_LuxR; 1.
DR SMART; SM00421; HTH_LuxR; 1.
DR PROSITE; PS00622; HTH_LuxR_FAMILY; 1.
KW Transcription regulation; DNA-binding; Activator; Quorum sensing;
KW Autoinducer synthesis; Complete proteome.
FT DNA_BIND 193 212 H-T-H MOTIF (POTENTIAL).
SQ SEQUENCE 236 AA; 25926 MW; 4F11E733A4890F5F CRC64;

Query Match 46.1%; Score 41; DB 1; Length 236;
Best Local Similarity 87.5%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EVLCWTWE 9
||||| |
Db 182 EVLCWTGE 189

RESULT 15
SLR2_RALSO
ID SLR2_RALSO STANDARD; PRT; 236 AA.
AC O30919;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transcriptional activator protein solR.
GN SOLR.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AW1;
RX MEDLINE=98037508; PubMed=9371457;
RA Flavie A.B., Ganova-Raeva L.M., Schell M.A., Denny T.P.;
RT "Hierarchical autoinduction in Ralstonia solanacearum: control of
acyl-homoserine lactone production by a novel autoregulatory system
responsive to 3-hydroxypalmitic acid methyl ester.";
RL J. Bacteriol. 179:7089-7097(1997).
CC -!- SIMILARITY: BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL
REGULATORS. AUTOINDUCER REGULATED SUBFAMILY.

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CC EMBL; AF021840; AAC45947.1; -.
DR InterPro; IPR005143; Autoind_bind.
DR InterPro; IPR000792; HTH_LuxR.
DR Pfam; PF00196; GerE; 1.
DR Pfam; PF03472; Autoind_bind; 1.
DR PRINTS; PR00038; HTHLUXR.
DR ProDom; PD000307; HTH_LuxR; 1.
DR SMART; SM00421; HTH_LuxR; 1.
DR PROSITE; PS00622; HTH_LuxR_FAMILY; 1.
KW Transcription regulation; DNA-binding; Activator;
KW Quorum sensing; Autoinducer synthesis.
FT DNA_BIND 193 212 H-T-H MOTIF (POTENTIAL).
SQ SEQUENCE 236 AA; 25884 MW; B2F646DA2EE2602D CRC64;

Query Match 46.1%; Score 41; DB 1; Length 236;
Best Local Similarity 87.5%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EVLCWTWE 9
||||| |
Db 182 EVLCWTGE 189

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